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6/26/02

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/081,218

DATE: 03/12/2002

TIME: 09:57:00

Input Set : N:\Crf3\RULE60\10081218.raw

Output Set: N:\CRF3\03122002\J081218.raw

## SEQUENCE LISTING

ENTERED

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: SHIBAYAMA, SHIRO

6 HIRANO, ATSUSHI

7 OHNO, HIROYUKI

9 (ii) TITLE OF INVENTION: A NOVEL POLYPEPTIDE AND DNAS ENCODING IT

11 (iii) NUMBER OF SEQUENCES: 6

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK &amp; SEAS

15 (B) STREET: 2100 Pennsylvania Avenue, N.W.

16 (C) CITY: Washington

17 (D) STATE: D.C.

18 (E) COUNTRY: U.S.A.

19 (F) ZIP: 20037-3202

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

27 (vi) CURRENT APPLICATION DATA:

C--&gt; 28 (A) APPLICATION NUMBER: US/10/081,218

C--&gt; 29 (B) FILING DATE: 25-Feb-2002

30 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: US/09/246,355

34 (B) FILING DATE:

36 (A) APPLICATION NUMBER: US/08/852,811

37 (B) FILING DATE: 07-MAY-1997

39 (A) APPLICATION NUMBER: 08/439,457

40 (B) FILING DATE:

42 (A) APPLICATION NUMBER: JP 123155/1994

43 (B) FILING DATE: 12-MAY-1994

45 (ix) TELECOMMUNICATION INFORMATION:

46 (A) TELEPHONE: (202)293-7060

47 (B) TELEFAX: (202)293-7860

48 (C) TELEX: 6491103

51 (2) INFORMATION FOR SEQ ID NO: 1:

53 (i) SEQUENCE CHARACTERISTICS:

54 (A) LENGTH: 205 amino acids

55 (B) TYPE: amino acid

56 (D) TOPOLOGY: linear

58 (ii) MOLECULE TYPE: protein

63 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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66 Met Gly Thr Ala Gly Ala Met Gln Leu Cys Trp Val Ile Leu Gly Phe
67 -24 -20 -15 -10
68 Leu Leu Phe Arg Gly His Asn Ser Gln Pro Thr Met Thr Gln Thr Ser
69 -5 1 5
71 Ser Ser Gln Gly Gly Leu Gly Gly Leu Ser Leu Thr Thr Glu Pro Val
72 10 15 20
74 Ser Ser Asn Pro Gly Tyr Ile Pro Ser Ser Glu Ala Asn Arg Pro Ser
75 25 30 35 40
77 His Leu Ser Ser Thr Gly Thr Pro Gly Ala Gly Val Pro Ser Ser Gly
78 45 50 55
80 Arg Asp Gly Gly Thr Ser Arg Asp Thr Phe Gln Thr Val Pro Pro Asn
81 60 65 70
83 Ser Thr Thr Met Ser Leu Ser Met Arg Glu Asp Ala Thr Ile Leu Pro
84 75 80 85
86 Ser Pro Thr Ser Glu Thr Val Leu Thr Val Ala Ala Phe Gly Val Ile
87 90 95 100
89 Ser Phe Ile Val Ile Leu Val Val Val Val Ile Ile Leu Val Gly Val
90 105 110 115 120
92 Val Ser Leu Arg Phe Lys Cys Arg Lys Ser Lys Glu Ser Glu Asp Pro
93 125 130 135
95 Gln Lys Pro Gly Ser Ser Gly Leu Ser Glu Ser Cys Ser Thr Ala Asn
96 140 145 150
98 Gly Glu Lys Asp Ser Ile Thr Leu Ile Ser Met Lys Asn Ile Asn Met
99 155 160 165
101 Asn Asn Gly Lys Gln Ser Leu Ser Ala Glu Lys Val Leu
102 170 175 180
104 (2) INFORMATION FOR SEQ ID NO: 2:
106 (i) SEQUENCE CHARACTERISTICS:
107 (A) LENGTH: 618 base pairs
108 (B) TYPE: nucleic acid
109 (C) STRANDEDNESS: single
110 (D) TOPOLOGY: linear
112 (ii) MOLECULE TYPE: cDNA to mRNA
117 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
119 ATGGGCACCG CAGGAGCCAT GCAGCTGTGC TGGGTGATCC TGGGCTTCCT CCTGTTCCGA 60
121 GGCCACAACCT CCCAGCCCAC AATGACCCAG ACCTCTAGCT CTCAGGGAGG CCTTGGCGGT 120
123 CTAAGTCTGA CCACAGAGCC AGTTTCTTCC AACCCAGGAT ACATCCCTTC CTCAGAGGCT 180
125 AACAGGCCAA GCCATCTGTC CAGCACTGGT ACCCCAGGCG CAGGTGTCCC CAGCAGTGGA 240
127 AGAGACGGAG GCACAAGCAG AGACACATTT CAAACTGTTT CCCCCAATTC AACCACCATG 300
129 AGCCTGAGCA TGAGGGAAGA TGCGACCATC CTGCCCAGCC CCACGTCAGA GACTGTGCTC 360
131 ACTGTGGCTG CATTTGGTGT TATCAGCTTC ATTGTCATCC TGGTGGTTGT GGTGATCATC 420
133 CTAGTTGGTG TGGTCAGCCT GAGGTTCAAG TGTCGGAAGA GCAAGGAGTC TGAAGATCCC 480
135 CAGAAACCTG GGAGTTCAGG GCTGTCTGAA AGCTGCTCCA CAGCCAATGG AGAGAAAGAC 540
137 AGCATCACCC TTATCTCCAT GAAGAACATC AACATGAATA ATGGCAAACA AAGTCTCTCA 600
139 GCAGAGAAGG TTCTTTAA 618
141 (2) INFORMATION FOR SEQ ID NO: 3:
143 (i) SEQUENCE CHARACTERISTICS:
144 (A) LENGTH: 983 base pairs
145 (B) TYPE: nucleic acid

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146          (C) STRANDEDNESS: single
147          (D) TOPOLOGY: linear
149      (ii) MOLECULE TYPE: cDNA to mRNA
154      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
156 GCCTGCCCGC CACATACCCA GCTGACATGG GCACCGCAGG AGCCATGCAG CTGTGCTGGG      60
158 TGATCCTGGG CTTCTCTCTG TTCCGAGGCC ACAACTCCCA GCCCACAATG ACCCAGACCT      120
160 CTAGCTCTCA GGGAGGCCTT GGCGGTCTAA GTCTGACCAC AGAGCCAGTT TCTTCCAACC      180
162 CAGGATACAT CCCTTCTCTA GAGGCTAACA GGCCAAGCCA TCTGTCCAGC ACTGGTACCC      240
164 CAGGCGCAGG TGTCCCCAGC AGTGAAGAG ACGGAGGCAC AAGCAGAGAC ACATTTCAAA      300
166 CTGTTCCCCC CAATTCAACC ACCATGAGCC TGAGCATGAG GGAAGATGCG ACCATCCTGC      360
168 CCAGCCCCAC GTCAGAGACT GTGCTCACTG TGGCTGCATT TGGTGTATC AGCTTCATTG      420
170 TCATCCTGGT GGTGTGTGTG ATCATCCTAG TTGGTGTGGT CAGCCTGAGG TTCAAGTGTC      480
172 GGAAGAGCAA GGAGTCTGAA GATCCCCAGA AACCTGGGAG TTCAGGGCTG TCTGAAAGCT      540
174 GCTCCACAGC CAATGGAGAG AAAGACAGCA TCACCCTTAT CTCCATGAAG AACATCAACA      600
176 TGAATAATGG CAAACAAAGT CTCTCAGCAG AGAAGGTTCT TTAAGGCAA CTTTGGGTCC      660
178 CCATGAGTCC AAGGATGATG CAGCTGCCCT GTGACTACAA GGAGGAAGAG ATGGAATTAG      720
180 TAGAGGCAAT GAACCACATG TAAATTATTT TATTGTTTCA TGTCTGCTTC TAGATCTAAA      780
182 GGACACTAGC ATTGCCCCAG ATCTGGGAGC AAGCTACCAA CAGGGGAGAC TCTTTCCTGT      840
184 ATGGACAGCT GCTGTGGAAG TACTGCCTGC TTCTCCCACC TCCTCAGAGC CACAGGAAAG      900
186 AGGAGGTGAC AGAGAGAGAG CAAGGAAAGT GATGAGGTGG ATTGATACTT TCTACTTTGC      960
188 ATTAATAATTA TTTTCTAGCC TGC                                          983
190 (2) INFORMATION FOR SEQ ID NO: 4:
192      (i) SEQUENCE CHARACTERISTICS:
193          (A) LENGTH: 983 base pairs
194          (B) TYPE: nucleic acid
195          (C) STRANDEDNESS: single
196          (D) TOPOLOGY: linear
198      (ii) MOLECULE TYPE: cDNA to mRNA
200      (vi) ORIGINAL SOURCE:
201          (A) ORGANISM: Homo sapiens
202          (H) CELL LINE: endothelial cell line of umbilical cord vein
204      (ix) FEATURE:
205          (A) NAME/KEY: CDS
206          (B) LOCATION: 27..644
207          (C) IDENTIFICATION METHOD: by similarity to some other pattern
209      (ix) FEATURE:
210          (A) NAME/KEY: sig_peptide
211          (B) LOCATION: 27..98
212          (C) IDENTIFICATION METHOD: by similarity with known sequence or
213 to an established consensus
215      (ix) FEATURE:
216          (A) NAME/KEY: misc_feature
217          (B) LOCATION: 381..464
218          (C) IDENTIFICATION METHOD: by similarity with known sequence or
219 to an established consensus
221      (ix) FEATURE:
222          (A) NAME/KEY: mat_peptide
223          (B) LOCATION: 99..641
224          (C) IDENTIFICATION METHOD: by similarity with known sequence or

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225 to an established consensus

227 (ix) FEATURE:

228 (A) NAME/KEY: misc\_feature

229 (B) LOCATION: 312..320

230 (C) IDENTIFICATION METHOD: by similarity with known sequence or

231 to an established consensus

234 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

236 GCCTGCCCGC CACATACCCA GCTGAC ATG GGC ACC GCA GGA GCC ATG CAG CTG 53

237 Met Gly Thr Ala Gly Ala Met Gln Leu

238 -24 -20

240 TGC TGG GTG ATC CTG GGC TTC CTC CTG TTC CGA GGC CAC AAC TCC CAG 101

241 Cys Trp Val Ile Leu Gly Phe Leu Leu Phe Arg Gly His Asn Ser Gln

242 -15 -10 -5 1

244 CCC ACA ATG ACC CAG ACC TCT AGC TCT CAG GGA GGC CTT GGC GGT CTA 149

245 Pro Thr Met Thr Gln Thr Ser Ser Ser Gln Gly Gly Leu Gly Leu

246 5 10 15

248 AGT CTG ACC ACA GAG CCA GTT TCT TCC AAC CCA GGA TAC ATC CCT TCC 197

249 Ser Leu Thr Thr Glu Pro Val Ser Ser Asn Pro Gly Tyr Ile Pro Ser

250 20 25 30

252 TCA GAG GCT AAC AGG CCA AGC CAT CTG TCC AGC ACT GGT ACC CCA GGC 245

253 Ser Glu Ala Asn Arg Pro Ser His Leu Ser Ser Thr Gly Thr Pro Gly

254 35 40 45

256 GCA GGT GTC CCC AGC AGT GGA AGA GAC GGA GGC ACA AGC AGA GAC ACA 293

257 Ala Gly Val Pro Ser Ser Gly Arg Asp Gly Gly Thr Ser Arg Asp Thr

258 50 55 60 65

260 TTT CAA ACT GTT CCC CCC AAT TCA ACC ACC ATG AGC CTG AGC ATG AGG 341

261 Phe Gln Thr Val Pro Pro Asn Ser Thr Thr Met Ser Leu Ser Met Arg

262 70 75 80

264 GAA GAT GCG ACC ATC CTG CCC AGC CCC ACG TCA GAG ACT GTG CTC ACT 389

265 Glu Asp Ala Thr Ile Leu Pro Ser Pro Thr Ser Glu Thr Val Leu Thr

266 85 90 95

268 GTG GCT GCA TTT GGT GTT ATC AGC TTC ATT GTC ATC CTG GTG GTT GTG 437

269 Val Ala Ala Phe Gly Val Ile Ser Phe Ile Val Ile Leu Val Val Val

270 100 105 110

272 GTG ATC ATC CTA GTT GGT GTG GTC AGC CTG AGG TTC AAG TGT CGG AAG 485

273 Val Ile Ile Leu Val Gly Val Val Ser Leu Arg Phe Lys Cys Arg Lys

274 115 120 125

276 AGC AAG GAG TCT GAA GAT CCC CAG AAA CCT GGG AGT TCA GGG CTG TCT 533

277 Ser Lys Glu Ser Glu Asp Pro Gln Lys Pro Gly Ser Ser Gly Leu Ser

278 130 135 140 145

280 GAA AGC TGC TCC ACA GCC AAT GGA GAG AAA GAC AGC ATC ACC CTT ATC 581

281 Glu Ser Cys Ser Thr Ala Asn Gly Glu Lys Asp Ser Ile Thr Leu Ile

282 150 155 160

284 TCC ATG AAG AAC ATC AAC ATG AAT AAT GGC AAA CAA AGT CTC TCA GCA 629

285 Ser Met Lys Asn Ile Asn Met Asn Asn Gly Lys Gln Ser Leu Ser Ala

286 165 170 175

288 GAG AAG GTT CTT TAA AAGCAACTTT GGGTCCCAT GAGTCCAAGG ATGATGCAGC 684

289 Glu Lys Val Leu \*

290 180

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292 TGGCCTGTGA CTACAAGGAG GAAGAGATGG AATTAGTAGA GGCAATGAAC CACATGTAAA      744
294 TTATTTTATT GTTTCATGTC TGCTTCTAGA TCTAAAGGAC ACTAGCATTG CCCCAGATCT      804
296 GGGAGCAAGC TACCAACAGG GGAGACTCTT TCCTGTATGG ACAGCTGCTG TGGAAATACT      864
298 GCCTGCTTCT CCCACCTCCT CAGAGCCACA GGAAAGAGGA GGTGACAGAG AGAGAGCAAG      924
300 GAAAGTGATG AGGTGGATTG ATACTTTCTA CTTTGCATTA AAATTATTTT CTAGCCTGC      983
302 (2) INFORMATION FOR SEQ ID NO: 5:
304     (i) SEQUENCE CHARACTERISTICS:
305         (A) LENGTH: 56 base pairs
306         (B) TYPE: nucleic acid
307         (C) STRANDEDNESS: double
308         (D) TOPOLOGY: linear
W--> 310     (ii) MOLECULE TYPE: DNA (synthetic)
315     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
317 GGAGCTCGTC GACAGATCTG AATTCATAT GCCCGGGGCG GCCGCACTAG TGGTAC      56
319 (2) INFORMATION FOR SEQ ID NO: 6:
321     (i) SEQUENCE CHARACTERISTICS:
322         (A) LENGTH: 56 base pairs
323         (B) TYPE: nucleic acid
324         (C) STRANDEDNESS: double
325         (D) TOPOLOGY: linear
W--> 327     (ii) MOLECULE TYPE: DNA (synthetic)
332     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
334 CACTAGTGCG GCCGCCCCGG GCATATGGAA TTCAGATCTG TCGACGAGCT CCTGCA      56

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/081,218

DATE: 03/12/2002

TIME: 09:57:01

Input Set : N:\Crf3\RULE60\10081218.raw

Output Set: N:\CRF3\03122002\J081218.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:310 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5

L:327 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6